33. An isolated polypeptide comprising a fragment of at least 7 consecutive amino acids of the polypeptide as claimed in any one of claims 30 to 32, wherein the fragment comprises an epitope.

34. The polypeptide of claim 33, wherein the fragment is immunogenic.

35. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide that has at least 75% identity to the amino acid sequence of SEQ ID NO:42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70 or 72 over its entire length; or a nucleotide sequence complementary to said isolated polynucleotide.

36. An isolated polynucleotide comprising a nucleotide sequence that has at least 75% identity to a nucleotide sequence, encoding a polypeptide of SEQ ID NO:42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70 or 72, over its entire length; or a nucleotide sequence complementary to said isolated polynucleotide.

37. An isolated polynucleotide which comprises a nucleotide sequence which has at least 75% identity to that of SEQ ID NO:41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69 or 71 over its entire length; or a nucleotide sequence complementary to said isolated polynucleotide.

38. The isolated polynucleotide as claimed in claim 35 in which the identity is at least 95% to SEQ ID NO:41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69 or 71 over its entire length.

39. The isolated polynucleotide as claimed in claim 36 in which the identity is at least 95% to SEQ ID NO:41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69 or 71 over its entire length.

40. The isolated polynucleotide as claimed in claim 37 in which the identity is at least 95% to SEQ ID NO:41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69 or 71 over its entire length.

41. An isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO:42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70 or 72.

42. An isolated polynucleotide comprising the polynucleotide of SEQ ID NO:41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69 or 71.

43. An isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO:42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70 or 72, obtainable by screening an appropriate library under stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO:41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69 or 71 or a fragment thereof.

44. An expression vector comprising an isolated polynucleotide according to any one of claims 35-43.

45. A recombinant live microorganism comprising an isolated polynucleotide according to any one of claims 35-43.

46. A host cell comprising the expression vector of claim 44 or a subcellular fraction or a membrane of said host cell.

47. A process for producing the polypeptide of claim 30 comprising the steps of culturing a host cell of claim 46 under conditions sufficient for the production of said polypeptide and recovering the polypeptide from the culture medium.

48. A process for expressing a polynucleotide of any one of claims 35-43 comprising transforming a host cell with an expression vector comprising at least one of said polynucleotides and culturing said host cell under conditions sufficient for expression of any one of said polynucleotides.

49. A vaccine composition comprising an effective amount of the polypeptide of claim 30 and a pharmaceutically acceptable carrier.

50. A vaccine composition comprising an effective amount of the polypeptide of claim 31 and a pharmaceutically acceptable carrier.

51. A vaccine composition comprising an effective amount of the polypeptide of claim 32 and a pharmaceutically acceptable carrier.

52. A vaccine composition comprising an effective amount of the polypeptide of claim 33 and a pharmaceutically acceptable carrier.

53. A vaccine composition comprising an effective amount of the polypeptide of claim 34 and a pharmaceutically acceptable carrier.

54. The vaccine composition of claim 49, wherein the polypeptide has an amino acid sequence selected from the group consisting of: SEQ ID NO:42, 46, 48, 50, 52, 54, 56, 58, 60 and 62.

55. A vaccine composition comprising an effective amount of the polynucleotide of any one of claims 35 to 43 and a pharmaceutically acceptable carrier.

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56. The vaccine composition according to any one of claims 49-55, wherein said composition comprises at least one other *Bordetella pertussis* antigen.

57. An antibody immunospecific for the amino acid sequence of claim 30 or 31.

58. An antibody immunospecific for the polypeptide of claim 32.

59. An antibody immunospecific for the fragment of claim 33.

60. An antibody immunospecific for the fragment of claim 34.

61. A method of diagnosing a *Bordetella pertussis* infection, comprising identifying a polypeptide as claimed claim 30, or an antibody that is immunospecific for said polypeptide, present within a biological sample from an animal suspected of having such an infection.

62. A method of diagnosing a *Bordetella pertussis* infection, comprising identifying a polypeptide as claimed claim 31, or an antibody that is immunospecific for said polypeptide, present within a biological sample from an animal suspected of having such an infection.

63. A method of diagnosing a *Bordetella pertussis* infection, comprising identifying a polypeptide as claimed claim 32, or an antibody that is immunospecific for said polypeptide, present within a biological sample from an animal suspected of having such an infection.

64. A method of diagnosing a *Bordetella pertussis* infection, comprising identifying a polypeptide as claimed claim 33, or an antibody that is immunospecific for said polypeptide, present within a biological sample from an animal suspected of having such an infection.

65. A method of diagnosing a *Bordetella pertussis* infection, comprising identifying a polypeptide as claimed claim 34, or an antibody that is immunospecific for said polypeptide, present within a biological sample from an animal suspected of having such an infection.

66. A therapeutic composition useful in treating humans with *Bordetella pertussis* disease comprising at least one antibody directed against the polypeptide of claim 30 and a suitable pharmaceutical carrier.

67. A therapeutic composition useful in treating humans with *Bordetella pertussis* disease comprising at least one antibody directed against the polypeptide of claim 31 and a suitable pharmaceutical carrier.

68. A therapeutic composition useful in treating humans with *Bordetella pertussis* disease comprising at least one antibody directed against the polypeptide of claim 32 and a suitable pharmaceutical carrier.

69. A therapeutic composition useful in treating humans with *Bordetella pertussis* disease comprising at least one antibody directed against the polypeptide of claim 33 and a suitable pharmaceutical carrier.

70. A therapeutic composition useful in treating humans with *Bordetella pertussis* disease comprising at least one antibody directed against the polypeptide of claim 34 and a suitable pharmaceutical carrier.

71. A kit for diagnosing infection with *B. pertussis* bacteria in a human comprising a polynucleotide of claims 35-43.

72. A kit for diagnosing infection with *B. pertussis* bacteria in a human comprising a polypeptide of claim 30.

73. A kit for diagnosing infection with *B. pertussis* bacteria in a human comprising a polypeptide of claim 31.

74. A kit for diagnosing infection with *B. pertussis* bacteria in a human comprising a polypeptide of claim 32.

75. A kit for diagnosing infection with *B. pertussis* bacteria in a human comprising a polypeptide of claim 33.

76. A kit for diagnosing infection with *B. pertussis* bacteria in a human comprising a polypeptide of claim 34.

77. A method of identifying virulence genes from a pathogenicity island containing a type III secretion system from pathogenic strains of bacteria, comprising:

designing degenerate PCR primers complementary to well-conserved regions specific to the LcrD polypeptide of *Yersinia*;

amplifying the polynucleotide containing the DNA sequence between (and including the DNA sequence of) the primers of *lcrD*-like genes present in said pathogenic strain of bacteria;

sequencing the *lcrD*-like gene;

determining whether the DNA sequence is more homologous: to the virulence-associated family of *lcrD*-like genes, or to the flagellar-associated family of *lcrD*-like genes; and